IN THE SPECIFICATION:

Please replace the paragraph at page 10, line 26 to page 11, line 6, as follows:

~~Fig. 1 shows~~ **Figs. 1A-1B** show the pedigree of the individuals used in the genetic linkage studies. Under each individual is an ID number, the z-score for spinal BMD, and the allele calls for the critical markers on chromosome 11. Solid symbols represent "affected" individuals. Symbols containing "N" are "unaffected" individuals. DNA from 37 individuals was genotyped. Question marks denote unknown genotypes or individuals who were not genotyped.

Please replace the paragraph at page 11, lines 6-17, as follows:

~~Fig. 2 depicts~~ **Figs. 2A-2B** depict the BAC/STS content physical map of the HBM region in 11q13.3. STS markers derived from genes, ESTs, microsatellites, random sequences, and BAC endsequences are denoted above the long horizontal line. For markers that are present in GDB the same nomenclature has been used. Locus names (D11S####) are listed in parentheses after the primary name if available. STSs derived from BAC endsequences are listed with the BAC name first followed by L or R for the left and right end of the clone, respectively. The two large arrows indicate the genetic markers that define the HBM critical region. The horizontal lines below the STSs indicate BAC clones identified by PCR-based screening of a nine-fold coverage BAC library. Open circles indicate that the marker did not amplify the corresponding BAC library address during library screening. Clone names use the following convention: B for BAC, the plate, row and column address, followed by -H indicating the HBM project (i.e., B36F16-H).

Please replace the paragraph at page 12, lines 13-17, as follows:

~~Figs. 6A-6E~~ **Figs. 6A-6J** are the nucleotide and amino acid sequences of the wild-type gene, Zmax1. The location for the base pair substitution at nucleotide 582, a guanine to thymine, is underlined. This allelic variant is the HBM gene. The HBM gene encodes for a protein with an amino acid substitution of glycine to valine at position 171. The 5' untranslated region (UTR) boundaries bases 1 to 70, and the 3' UTR boundaries bases 4916-5120.

Please replace the paragraph at page 12, lines 22-23, as follows:

~~Fig. 10 is~~ **Figs. 10A-10B** are the cellular localization of mouse Zmax1 by *in situ* hybridization at 100X magnification using sense and antisense probes.

Please replace the paragraph at page 12, lines 24-25, as follows:

~~Fig. 11 is~~ **Figs. 11A-11B** are the cellular localization of mouse Zmax1 by *in situ* hybridization at 400X magnification using sense and antisense probes.

Please replace the paragraph at page 12, line 26 to page 13, line 1, as follows:

~~Fig. 12 is~~ **Figs. 12A-12B** are the cellular localization of mouse Zmax1 by *in situ* hybridization of osteoblasts in the endosteum at 400X magnification using sense and antisense probes.

Please replace the paragraph at page 108, line 19 to page 109, line 2, as follows:

The present invention describes DNA sequences derived from two BAC clones from the HBM gene region, as evident in Table 6 below, which is an assembly of these clones. Clone b200e21-h (ATCC No. ~~980812~~ 98628; SEQ ID NOS: 10-11) was deposited at the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, VA 20110-2209 U.S.A., on December 30, 1997. Clone b527d12-h (ATCC No. ~~980720~~ 98907; SEQ ID NOS: 5-9) was deposited at the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, VA 20110-2209 U.S.A., on October 2, 1998. These sequences are unique reagents that can be used by one skilled in the art to identify DNA probes for the Zmax1 gene, PCR primers to amplify the gene, nucleotide polymorphisms in the Zmax1 gene, or regulatory elements of the Zmax1 gene.

Please replace Table 6 at page 109 as follows:

TABLE 6

Contig	ATCC No.	SEQ ID NO.	Length (base pairs)
b527d12-h_contig302G	~~980720~~ 98907	5	3096
b527d12-h_contig306G	~~980720~~ 98907	6	26928
b527d12-h_contig307G	~~980720~~ 98907	7	29430
b527d12-h_contig308G	~~980720~~ 98907	8	33769
b527d12-h_contig309G	~~980720~~ 98907	9	72049
b200e21-h_contig1	~~980812~~ 98628	10	8705
b200e21-h_contig4	~~980812~~ 98628	11	66933